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EXAMINER	
NEGIN, RUSSELL SCOTT	
ART UNIT	**PAPER NUMBER**
1631	

NOTIFICATION DATE	DELIVERY MODE
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

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Office Action Summary	Application No.	Applicant(s)	
	10/817,244	YAKHINI ET AL.	
	Examiner	Art Unit	
	Russell S. Negin	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *19 July 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-56 and 80-100* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-56 and 80-100* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *6/11/2007*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Comments

Applicants' amendments and request for reconsideration in the communication filed on 19 July 2007 are acknowledged and the amendments are entered.

Claims 1-56 and 80-100 are pending and examined in the instant Office action.

Specification

The objection to the disclosure because it contains an embedded hyperlink and/or other form of browser-executable code is withdrawn in view of amendments to the specification filed by applicant on 19 July 2007.

Claim Objections

The objections to claims 20 and 55 because of the informalities are withdrawn in view of amendments filed by applicant to the set of claims on 19 July 2007.

Claim Rejections - 35 USC § 112

The following 35 U.S.C. 112 Rejections are newly applied:

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-56 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter

which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The following negative limitation that has been added to claim 1, line 3, which states, "importing arbitrary gene- and protein-related data *that has not been mapped to a chromosome map...*" does not have support in the original disclosure. Neither the section of the disclosure nor the section of the disclosure indicated by applicants in the Remarks shows and states the negative limitation of data that has not been mapped to a chromosome map.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 34-56 and 80-100 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In line 6 of claim 34 and line 16 of claim 80 have the phrase, "tissue exhibiting a known abnormality," where it is unclear to whom, when, and where the abnormality is known.

Claim Rejections - 35 USC § 102

The rejections of claims 1-3, 7, 12-15 and 27-28 under 35 U.S.C. 102(b) as being anticipated by Ben-Dor et al. [Genome Research, 2000, volume 10, pages 365-378] are withdrawn in view of amendments filed by applicant on 19 July 2007.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #1:

Claims 1-3, 7, 12-15, and 27-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. [Genome Research, 2000, volume 10, pages 365-378].

Claim 1 is drawn to a method for overlaying gene- or protein-related data on chromosome maps, said method comprising the steps of:

--importing arbitrary gene- or protein-related data that has not been mapped to a chromosome map and having identifiers for determining genetic loci of genes to which said arbitrary gene-related data are associated;

--matching the identifiers with predefined identifiers on at least one of the chromosome maps; and

--displaying the arbitrary gene- or protein related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene or protein-related data are located, wherein said importing, reading, matching and displaying are all automated steps.

The article of Ben-Dor et al., entitled, "RHO-Radiation Hybrid Ordering" states in its abstract:

> Radiation hybrid (RH) mapping is a somatic cell technique that is used for ordering markers along a chromosome and estimating the physical distances between them. With the advent of this mapping technique, analyzing the experimental data is becoming a challenging and demanding computational task. In this paper we present the software package RHO (radiation hybrid ordering). This package implements a number of heuristics to order genomic markers along a chromosome, given as input the results of an RH experiment.

The gene data is imported from the Whitehead Institute (the external source) as stated in the lines bridging columns 1 and 2 of page 368 of Ben-Dor et al.:

> The RH data used to construct the maps was downloaded from the Whitehead Institute for Biomedical Research.

Identifiers are listed in Table 4 of page 371 of Ben-Dor et al. and the matching process is described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372:

> Different maps of the same chromosome give rise to different estimates of its total physical length. Shorter maps are generally viewed as more desirable ones. This transformation of probabilities to distances is implemented in RHMAPPER. Using this implementation, we conclude that the total physical length of chromosome 2 in our map is 3.88% shorter that in the

> WI framework map... The detailed differences between the two maps are depicted graphically in Figure 6. These map portions are drawn to scale.

Consequently, Figure 6 of Ben-Dor et al. maps the chromosome identifiers between the chromosome 2 map and the WI framework map. The data in Figure 6 of Ben-Dor et al. are spatially grouped on the chromosome map. There is a plurality of chromosome maps illustrated in Figure 6 of Ben-Dor et al.

Page 370 of Ben-Dor et al. devotes this technique for "A New Map of Chromosome 2," indicating that the relevant data has not already been mapped to a chromosome (i.e. it is a new chromosome map).

Ben-Dor et al. does not explicitly state that every step corresponding to the instant claim is automated. However, the court decision of In re Venner recites:

> In re Venner, 262 F.2d 91, 95, 120 USPQ 193, 194 (CCPA 1958) (Appellant argued that claims to a permanent mold casting apparatus for molding trunk pistons were allowable over the prior art because the claimed invention combined "old permanent-mold structures together with a timer and solenoid which automatically actuates the known pressure valve system to release the inner core after a predetermined time has elapsed." The court held that broadly providing an automatic or mechanical means to replace a manual activity which accomplished the same result is not sufficient to distinguish over the prior art.).

Consequently, it would obvious to automate a manual activity listed in Ben-Dor et al. corresponding to the instantly rejected claim to yield results more expeditiously and accurately.

Claim 2 is dependent from claim 1 with the additional limitation of further comprising interactive selection by a user of at least one data type to be displayed during said displaying.

Figure 6 of Ben-Dor et al. schematically diagrams the data types of the sequence identifiers.

Claim 3 depends from claim 1 with the additional limitation of further comprising spatially grouping said gene- or protein related data to correspond to spatial groupings of said associated genes on said at least one chromosome map.

Figure 6 of Ben-Dor et al. illustrates spatial groupings of chromosome maps and relations with WI framework maps.

Claim 7 is dependent from claim 1 with the additional limitation of maintaining focus and context of at least a portion of the display of said chromosome maps and gene or protein-related data.

Figure 6 of Ben-Dor et al. illustrates a plurality of chromosome maps with focuses on portions of each chromosome map.

Claim 12 is dependent from claim 1 with the additional limitation of further comprising accessing an external source of information relative to the data displayed, matching at least one of said identifiers with specific information in said external source, and displaying said specific information relative to said gene or protein-related data associated with said at least one identifier.

Figure 6 of Ben-Dor et al. illustrates matching data of chromosome maps with external sources, and displaying said information with an identifier.

Claim 13 is dependent from claim 1 with the additional limitation that the identifiers of said arbitrary gene or protein related data are selected from published gene identifiers and symbols.

Claim 14 is dependent from claim 13 with such a given list of symbol types.

The identifier symbols in Figure 6 of Ben-Dor et al. correspond to such required identifiers.

Claim 15 is dependent from claim 1 with the additional limitation that the matching comprises providing a relational database which stores a set of cross-referenced tables for matching said identifiers with said predefined identifiers.

Figure 6 of Ben-Dor et al. illustrates a relational database between chromosome maps and a WI framework map with the proper predefined identifiers.

Claim 27 is dependent from claim 1 with the additional limitation that said arbitrary gene or protein data is imported from a plurality of experiments.

Claim 28 is dependent from claim 27 with the additional limitation that said gene or protein data is displayed with regard to each of the plurality of experiments on a single display.

Figure 6 of Ben-Dor et al. illustrates such a plurality of graphs based on a plurality of experiments.

Response to Arguments:

Applicant's arguments filed 19 July 2007 have been fully considered but they are not persuasive.

Applicant has several argument concerning the Ben-Dor et al. reference on pages 16-17 of the Remarks.

First, applicant argues that the objective of the Ben-Dor et al. reference teaches a different objective than the instantly rejected set of claims. This is not persuasive because even assuming the Ben Dor et al. reference taught an objective distinct form the instant set of claims, it attaining this objective, Ben-Dor et al. conducted a method on which the instant set of claim can read.

Second applicant states the following on page 16 of the Remarks:

> Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

This argument is not persuasive because "looking up identifiers" is not mentioned in the instant claim. Markers are read an then placed adjacent to the chromosome maps.

Third, applicant states on page 16 of the Remarks:

> Fig. 6 of Ben-Dor et al... simply shows difference between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map.

This argument is not persuasive because Figure 6 of Ben-Dor et al. does display a chromosome map as stated in the caption of Figure 6. The claims as currently recited do not limit Figure 6 of Ben-Dor et al. from reading on the given claims.

35 U.S.C. 103 Rejection #2:

Claims 16, 18, 20-26, 29-33, and 55-56 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. as applied to claims 1-3, 7, 12-15, and 27-28 above in further view of Stanyon et al. [Cytogenetics and Cell Genetics, volume 84, 1999, pages 150-155].

Claim 16 is dependent from claim 1 with the additional limitation that the gene related data comprises a expression matrix.

Claim 18 is dependent from calim1 with the additional limitation that said arbitrary gene or protein-related data comprises a matrix of at least one microarray of gene data wherein each row of the matrix is associated with a particular gene and wherein said matching comprises reordering and spatial grouping of the rows based on matching the identifiers to the predefined identifiers.

Ben-Dor et al. as applied to claims 1-3, 7, 12-15, and 27-28 above does not teach the claimed matrix and heat map limitations of the instant claims.

The article of Stanyon et al., entitled, "Reciprocal chromosome painting shown that genomic rearrangement between rat and mouse proceeds ten times faster than between humans and cats," states in the first sentence of the abstract:

> Reciprocal chromosome painting between mouse and rat using complete chromosome probe sets of both species permitted us to assign chromosomal homology between these rodents.

The purpose of the study is explained on page 151, column 1, lines 7-10, which state:

> Reciprocal chromosome painting between rat and mouse allows a transfer of gene mapping data from mouse to rat and vice versa, thus aiding in both disease and genetic trait analyses.

The annotated chromosome maps of the rat and mouse are shown in Figures 3 and 4 of page 152 of Stanyon et al. The numbers annotations are used for the comparison of rat to mouse genetic homologies..

A matrix is shown which compares the expression data between mouse and rat on page 153 of Stanyon et al. in which similarities are scored by coloring the tiles in the matrices.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al. as applied to claims 1-3, 7, 12-15, and 27-28 above in view of the homology study of Stanyon et al. because while Ben-Dor et al. examines differences in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determining similarities between the genomes of different species to aid in disease and genetic trait analyses.

Claim 20 is dependent from claim 1 with the additional limitation of further comprising statistically assessing co-location values and displaying assessed co-location statistical significance along side said arbitrary gene-related data.

Claim 21 is dependent from claim 1 with the additional limitation of displaying said genetic information of the chromosome map of the respective genes.

The statistics of each row and column of the matrix are enumerated in numbers that border each row and column of the matrix in Figure 5 of Stanyon et al. These statistics represent the percent agreement between FISH and gene mapping. The

matrix is color coded according the expression data and the clusters of data are evaluated in the numbers bordering each column and row on the matrix.

Claim 22 is dependent from claim 21 with the additional limitation of having the data comprise annotations.

Claim 23 is dependent from claim 22 with the additional limitation that the annotations are related to gene otology.

Claim 24 is dependent from claim 21 with the additional limitation that the additional information is taken from relevance scores.

Claim 25 is dependent from claim 22 with the additional limitation that the additional limitation is displayed in matrix form.

Claim 26 is dependent from claim 21 wherein the arbitrary gene and protein data is displayed in a scatter plot format.

The statistics of each row and column of the matrix are enumerated in numbers that border each row and column of the matrix in Figure 5 of Stanyon et al. The squares in this scatter plot or matrix have numbers on them to indicate relevance with FISH. These statistics represent the percent agreement between FISH and gene mapping. The matrix is color coded according the expression data and the clusters of data are evaluated in the numbers bordering each column and row on the matrix.

Claim 29 is dependent from claim 21 with the limitation that the additional data comprises statistical data.

Statistical data is displayed along side the matrix shown in Figure 5 of Stanyon et al.

Claim 30 is dependent from claim 18 with the additional limitation that calculating values for each row and an auxiliary process for obtaining cluster data for said row vectors and displaying such data.

Claim 31 is dependent from claim 30 with the additional limitation that the matrix comprises a heat map.

Claim 32 is dependent from claim 30 with the additional limitation that the cluster data is displayed adjacent each matrix.

Claim 33 is dependent from claim 30 with the additional limitation that the cluster data is displayed in multiple columns.

Figure 5 of Stanyon et al. illustrates a matrix of results around the checker-board "heat map" or matrix.

Claims 55 and 56 are dependent from claim 1 with the additional limitation of selecting additional information related to one or more genes and displaying this information along the side of the matrix. Claim 56 lists the types of information that qualify as possible data.

Figure 5 of Stanyon et al. illustrates a matrix of annotations results around the checker-board "heat map" or matrix.

Response to Arguments:

Applicant's arguments filed 19 July 2007 have been fully considered but they are not persuasive.

First, applicant argues for the reasons above, that the Ben-Dor et al. reference is deficient. This is not found persuasive because, for the reasons discussed above, the Ben-Dor et al. reference is not deficient.

Second, applicant argues on page 18 of the Remarks:

> Figs. 3 and 4 are ideograms summarizing the hybridization results of the experiments of Stanyon et al. There is no disclosure or suggestion of generating these ideograms by the method recited in present claim 1. Further, the rat chromosomes are painted with mouse probes, and vice versa, and the comparisons are thus provided by directly analyzing the experimental data... Nor does Stanyon teach or suggest displaying an expression matrix adjacent a chromosome map.

This argument is not persuasive because the study of Stanyon et al. is not an anticipatory prior art reference. When combined with the teaching of Ben-Dor et al., all of the limitations of the instantly rejected claims are addressed. In other words, while Stanyon et al. teaches matrix manipulation but not chromosome maps, per se, the study of Ben-Dor et al. teaches the recited chromosome mapping techniques but not the matrix manipulation techniques. When Ben-Dor et al. and Stanyon et al. are used together, both elements of the instant claims are addressed.

35 U.S.C. 103 Rejection #3:

Claims 4-6 and 8-11 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. as applied to claims 1-3, 7, 12-15, and 27-28 above in view of Koleszar et al. [US Patent 6,519,583].

Claim 4-6 and 8-11 are dependent from claim 1 with the additional features of displaying the genetic data is a specific means wherein each claim identifies a separate feature used to display the data.

Ben-Dor et al. as applied to claims 1-3, 7, 12-15, and 27-28 above does not teach the required display techniques.

The invention of Koleszar et al., entitled, "Graphical viewer for biomolecular sequence data," states in the abstract:

> Disclosed are methods, media and systems for graphically displaying computer-based biomolecular sequence information. Generally, biomolecular sequence information may be graphically depicted in a variety of different forms in accordance with the present invention. The sequence information may be composed of nucleotide or amino acid sequence information or both. The graphical depictions may be in several different formats providing different information relating to the sequences, and may be displayed in one or more screens of a computer user interface.

Figure 4A has the ability to zoom in on regions or zooming out and compressing regions of the genomic sequence of interest as is illustrated on the toolbar of the schematic with pop-up buttons to control the viewing of the features.

The purpose of Koleszar et al. in explained in column 2, lines 5-9, which states:

> Accordingly, the development if a display tool which allows a user to clearly and effectively display gene loci information for a given organism or organisms and/or other biomolecular sequences in desirable.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify Ben-Dor et al. as applied to claims 1-3, 7, 12-15, and 27-28 above by use of Koleszar et al., because Koleszar et al. has the advantage of displaying the genomic data of Ben-Dor et al. in a more convenient and user-friendly format.

Response to Arguments:

Applicant's arguments filed 19 July 2007 have been fully considered but they are not persuasive.

First, applicant argues for the reasons above, that the Ben-Dor et al. reference is deficient. This is not found persuasive because, for the reasons discussed above, the Ben-Dor et al. reference is not deficient.

Second, applicant argues on page 20 of the Remarks that Koleszar et al. does not teach the limitations of a chromosome map as disclosed in Ben-Dor et al. Additionally, Ben-Dor et al. does not disclose the required displays.

This argument is not persuasive because the study of Koleszar et al. is not an anticipatory prior art reference. When combined with the teaching of Ben-Dor et al., all of the limitations of the instantly rejected claims are addressed. In other words, while Koleszar et al. teaches the required display of sequence information but not chromosome maps, per se, the study of Ben-Dor et al. teaches the recited chromosome mapping techniques but not the matrix manipulation techniques. When Ben-Dor et al. and Koleszar et al. are used together, both elements of the instant claims are addressed.

35 U.S.C. 103 Rejection #4:

Claims 17 and 19 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Stanyon et al. as applied to claims 16, 18, 20-26, 29-33, and 55-56 above in view of Singer et al. [US Patent 5,866,331].

Claim 17 is dependent from claim 16 with the additional limitation of having a plurality of matrices.

Claim 19 is dependent from claim 18 with the additional limitation of comprising a heat map in the plurality of matrices.

Ben-Dor et al. in view of Stanyon et al. as applied to claims 16, 18, 20-26, 29-33, and 55-56 above fails to teach heat maps on a plurality of matrices.

The invention of Singer et al., entitled, "Single molecule detection by in situ hybridization," states that its purpose is to use cell microscopy, biology, and digital imaging to better detect shorter target sequences. As is stated in column 4, lines 49-51, "As few as five fluorochromes on a single probe provide a sufficiently strong signal for a detection of that single probe."

Figures 2A and 2B illustrate a plurality of heat maps used to detect hybridizations to nucleotide probes.

It would have been obvious at the time of the instant invention for someone of ordinary skill in the art to modify the radiation hybridization ordering study of Ben-Dor et al. as applied to claims 16, 18, 20-26, 29-33, and 55-56 above by use of the heat maps shown in Singer et al. because while Ben-Dor et al. generate the generic maps used to assess chromosomal topology, Singer et al. uses advanced mapping techniques to better detect hybridization to short target sequences.

Response to Arguments:

Applicant's arguments filed 19 July 2007 have been fully considered and they are persuasive. Upon addition of the study of Stanyon et al. to the instant 35 U.S.C. 103 rejection, this rejection becomes proper.

Conclusion

No Claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the central PTO Fax Center. The faxing of such pages must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993)(See 37 CFR § 1.6(d)). The Central PTO Fax Center Number is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Negin, Ph.D., whose telephone number is (571) 272-1083. The examiner can normally be reached on Monday-Friday from 7am to 4pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Supervisor, Marjorie Moran, Supervisory Patent Examiner, can be reached at (571) 272-0720.

Information regarding the status of the application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information on the PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/Shubo (Joe) Zhou/

RSN
27 September 2007

SHUBO (JOE) ZHOU, PH.D.
PRIMARY EXAMINER